



## SEQUENCE LISTING

<110> Caput, Daniel  
Ferrara, Pascual  
Laurent, Patrick  
Vita, Natalio

<120> IL-13 RECEPTOR

<130> IVD924

<140> 09/077,817

<141> 1998-09-14

<150> PCT/FR96/01756

<151> 1996-11-07

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<170> PatentIn Ver. 2.0

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<212> DNA

<213> Homo sapiens

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TTCATCTTCA GACACCGAGA TAAAAGTTAA CCCTCCTCAG GATTTTGAGA TAGTGGATCC 180

CGGATACTTA GGTTATCTCT ATTTGCAATG GCAACCCCCA CTGTCTCTGG ATCATTTTAA 240

GGAATGCACA GTGGAATATG AACTAAAATA CCGAAACATT GGTAGTGAAA CATGGAAGAC 300

CATCATTACT AAGAATCTAC ATTACAAAGA TGGGTTTGAT CTTAACAAGG GCATTGAAGC 360

GAAGATACAC ACGCTTTTAC CATGGCAATG CACAAATGGA TCAGAAGTTC AAAGTTCCTG 420

GGCAGAAACT ACTTATTGGA TATCACCACA AGGAATTCCA GAAACTAAAG TTCAGGATAT 480

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ACTTCTTGAT ACCAATTACA ACTTGTTTTA CTGGTATGAG GGCTTGGATC ATGCATTACA 600

GTGTGTTGAT TACATCAAGG CTGATGGACA AAATATAGGA TGCAGATTTC CCTATTTGGA 660

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 35 40 45  
 Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser Leu Asp His Phe Lys Glu  
 50 55 60  
 Cys Thr Val Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr  
 65 70 75 80  
 Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp  
 85 90 95  
 Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln  
 100 105 110  
 Cys Thr Asn Gly Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr  
 115 120 125  
 Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp  
 130 135 140  
 Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly  
 145 150 155 160  
 Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu  
 165 170 175  
 Gly Leu Asp His Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly  
 180 185 190  
 Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys  
 195 200 205  
 Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg  
 210 215 220  
 Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro  
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 Lys Trp Ser Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Asp Tyr  
 260 265 270  
 Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr Leu Val Thr Ala Thr Val  
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 Glu Asn Glu Thr Tyr Thr Leu Lys Thr Thr Asn Glu Thr Arg Gln Leu  
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3  
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&lt;212&gt; DNA

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&lt;400&gt; 3

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 Glu Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu  
 85 90 95  
 Gln Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile  
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 115 120 125  
 Val Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys  
 130 135 140  
 Ser Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu  
 145 150 155 160  
 Tyr Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile  
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 Phe Arg Glu Gly Gln Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val  
 180 185 190

1  
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 Arg Val Lys Pro Asp Pro Pro His Ile Lys Asn Leu Ser Phe His Asn  
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 245 250 255  
 Cys Leu Phe Tyr Glu Val Glu Val Asn Asn Ser Gln Thr Glu Thr His  
 260 265 270  
 Asn Val Phe Tyr Val Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu  
 275 280 285  
 Arg Asn Val Glu Asn Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro  
 290 295 300  
 Asp Thr Leu Asn Thr Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys  
 305 310 315 320  
 Tyr Glu Asp Asp Lys Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile  
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 Gly Lys Lys Arg Asn Ser Thr Leu Tyr Ile Thr Met Leu Leu Ile Val  
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 Pro Val Ile Val Ala Gly Ala Ile Ile Val Leu Leu Leu Tyr Leu Lys  
 355 360 365  
 Arg Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile  
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 Phe Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys  
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 Pro Val Asn Phe Thr Ile Lys Val Thr Gly Leu Ala Gln Val Leu Leu  
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 Gln Trp Lys Pro Asn Pro Asp Gln Glu Gln Arg Asn Val Asn Leu Glu  
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 Tyr Gln Val Lys Ile Asn Ala Pro Lys Glu Asp Asp Tyr Glu Thr Arg  
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 Ile Thr Glu Ser Lys Cys Val Thr Ile Leu His Lys Gly Phe Ser Ala  
 85 90 95  
 Ser Val Arg Thr Ile Leu Gln Asn Asp His Ser Leu Leu Ala Ser Ser  
 100 105 110  
 Trp Ala Ser Ala Glu Leu His Ala Pro Pro Gly Ser Pro Gly Thr Ser  
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	210					215					220							
Arg	Pro	Phe	Asp	Gln	Leu	Phe	Ala	Leu	His	Ala	Ile	Asp	Gln	Ile	Asn			
225					230					235					240			
Pro	Pro	Leu	Asn	Val	Thr	Ala	Glu	Ile	Glu	Gly	Thr	Arg	Leu	Ser	Ile			
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		260						265						270				
Glu	Val	Lys	Ile	His	Asn	Thr	Arg	Asn	Gly	Tyr	Leu	Gln	Ile	Glu	Lys			
	275						280					285						
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Asp	Val	Gln	Val	Arg	Ala	Ala	Val	Ser	Ser	Met	Cys	Arg	Glu	Ala	Gly			
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Ile	Lys	Leu	Phe	Pro	Pro	Ile	Pro	Ala	Pro	Lys	Ser	Asn	Ile	Lys	Asp			
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Leu	Phe	Val	Thr	Thr	Asn	Tyr	Glu	Lys	Ala	Gly	Ser	Ser	Glu	Thr	Glu			
385					390					395					400			
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			20					25					30					
Val	Thr	Asn	Leu	Ser	Val	Ser	Val	Glu	Asn	Leu	Cys	Thr	Ile	Ile	Trp			
		35					40					45						
Thr	Trp	Ser	Pro	Pro	Glu	Gly	Ala	Ser	Pro	Asn	Cys	Thr	Leu	Arg	Tyr			
	50					55					60							
Phe	Ser	His	Phe	Asp	Asp	Gln	Gln	Asp	Lys	Lys	Ile	Ala	Pro	Glu	Thr			
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				85					90					95				

31  
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 130 135 140  
 Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr Tyr  
 145 150 155 160  
 Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr Arg  
 165 170 175  
 Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu Pro  
 180 185 190  
 Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn Ala Gly  
 195 200 205  
 Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr Val Lys  
 210 215 220  
 Pro Asp Pro Pro His Ile Lys His Leu Leu Leu Lys Asn Gly Ala Leu  
 225 230 235 240  
 Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys Leu Thr  
 245 250 255  
 Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn Ile Leu  
 260 265 270  
 Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg Asn Met  
 275 280 285  
 Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp Ala Val  
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 Tyr Thr Val Arg Val Arg Val Lys Thr Asn Lys Leu Cys Phe Asp Asp  
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 Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe Lys Glu  
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31  
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Cone

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<223> in SEQ ID NO. 12, which is a variant of SEQ ID NO. 2, the sequence VRCVTL is substituted for the 8 C-terminal amino acids of the human protein.

&lt;400&gt; 11

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&lt;210&gt; 12

&lt;211&gt; 378

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&lt;213&gt; Artificial sequence

&lt;220&gt;

<223> variant of SEQ ID NO. 2 in which the sequence VRCVTL is substituted for the 8 C-terminal amino acids of the human protein.

&lt;400&gt; 12

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Cys Thr Val Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr  
65 70 75 80  
Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp  
85 90 95  
Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln  
100 105 110  
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115 120 125  
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130 135 140  
Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly  
145 150 155 160  
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195 200 205  
  
Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg  
210 215 220  
Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro  
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Lys Trp Ser Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Asp Tyr  
260 265 270  
Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr Leu Val Thr Ala Thr Val  
275 280 285  
Glu Asn Glu Thr Tyr Thr Leu Lys Thr Thr Asn Glu Thr Arg Gln Leu

21  
Cont

290		295		300
Cys Phe Val Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly				
305		310		315
Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys Trp Glu Gly Glu Asp Leu				320
		325		330
Ser Lys Lys Thr Leu Leu Arg Phe Trp Leu Pro Phe Gly Phe Ile Leu				335
		340		345
Ile Leu Val Ile Phe Val Thr Gly Leu Leu Leu Arg Lys Pro Asn Thr				350
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Tyr Pro Lys Met Val Arg Cys Val Thr Leu				365
		370		375

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 <223> motif characteristic of the family of chemokine receptors to which the polypeptides of SEQ ID NO. 2 and SEQ NO. 4 belong. Xaa can be any amino acid.

<400> 13

Trp Ser Xaa Trp Ser  
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AATAAA 6

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Fl  
Cont